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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/902,460

DATE: 12/10/2001

TIME: 11:25:51

Input Set : N:\Crf3\RULE60\09902460.txt

Output Set: N:\CRF3\12102001\I902460.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: FIDDES, J.C.
 6 ABRAHAM, J.D.
 8 (ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
 9 FACTOR ANALOG
 11 (iii) NUMBER OF SEQUENCES: 69
 13 (iv) CORRESPONDENCE ADDRESS:
 14 (A) ADDRESSEE: MORRISON & FOERSTER
 15 (B) STREET: 755 PAGE MILL ROAD
 16 (C) CITY: Palo Alto
 17 (D) STATE: CA
 18 (E) COUNTRY: USA
 19 (F) ZIP: 94304-1018
 21 (v) COMPUTER READABLE FORM:
 22 (A) MEDIUM TYPE: Diskette
 23 (B) COMPUTER: IBM Compatible
 24 (C) OPERATING SYSTEM: Windows
 25 (D) SOFTWARE: FastSEQ for Windows Version 2.0b
 27 (vi) CURRENT APPLICATION DATA:
 C--> 28 (A) APPLICATION NUMBER: US/09/902,460
 C--> 29 (B) FILING DATE: 09-Jul-2001
 30 (C) CLASSIFICATION:
 32 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: 09/098,628
 34 (B) FILING DATE: 1998-06-16
 38 (viii) ATTORNEY/AGENT INFORMATION:
 39 (A) NAME: Lehnhardt, Susan K
 40 (B) REGISTRATION NUMBER: 33,943
 41 (C) REFERENCE/DOCKET NUMBER: 21900-20089.10
 43 (ix) TELECOMMUNICATION INFORMATION:
 44 (A) TELEPHONE: 650-813-5600
 45 (B) TELEFAX: 650-494-0792
 46 (C) TELEX: 706141
 49 (2) INFORMATION FOR SEQ ID NO: 1:
 51 (i) SEQUENCE CHARACTERISTICS:
 52 (A) LENGTH: 1969 base pairs
 53 (B) TYPE: nucleic acid
 54 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear
 57 (ii) MOLECULE TYPE: cDNA
 58 (ix) FEATURE:
 60 (A) NAME/KEY: Coding Sequence
 61 (B) LOCATION: 970...1434
 62 (D) OTHER INFORMATION:
 64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 66 AATTCATGCC TCTTCTCTC CTTTGTTGG TAGACGACTT CAGCCTCTGT CCTTAAATTT 60

ENTERED

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67 TAAAGTTTAT GCCCACTTG TACCCCTCGT CTTTGGTGA TTAGAGATT TTCAAAGCCT 120
68 GCTCTGACAC AGACTCTTCC TTGGATTGCA ACTTCTCTAC TTTGGGGTGG AAACGGCTTC 180
69 TCCGTTTTGA AACGCTAGCG GGGAAAAAAT GGGGGAGAAA GTTGAGTTA AACTTTTAAA 240
70 AGTTGAGTCA CGGCTGGTTG CGCACGAAAA GCCCCGCAGT GTGGAGAAAG CCTAAACGTG 300
71 GTTTGGGTGG TCGGGGGGTT GGGCGGGGGT GACTTTTGGG GGATAAGGGG CGGTGGAGCC 360
72 CAGGGAATGC CAAAGCCCTG CCGCGGCCCTC CGACGCGCGC CCCCCGCCCC TCGCCTCTCC 420
73 CCGCCCCCG ACTGAGGCCG GGCTCCCCGC CGGACTGATG TCGCGCGCTT GCGTGTGTG 480
74 GCCGAAGCCG CCGAACTCAG AGGCCGGCCC CAGAAAACCC GAGCGAGTAG GGGCGGCGC 540
75 GCAGGAGGGA GGAGAACTGG GGGCGCGGGA GGCTGGTGGG TGTGGGGGGT GGAGATGTAG 600
76 AAGATGTGAC GCCCGGGCCC GGCGGGTGCC AGATTAGCGG ACGGCTGCCC GCGGTTGCAA 660
77 CGGGATCCCG GGCGCTGCAG CTTGGGAGGC GGCTCTCCCC AGGCGGCGTC CGCGGAGACA 720
78 CCCATCTGTG AACCCAGGT CCGGGGCCGC CGGCTCGCCG CGCACCAGGG GCCGGCGGAC 780
79 AGAAGAGCGG CCGAGCGGCT CGAGGCTGGG GGACCGCGGG CGCGGCCGCG CGCTGCCGGG 840
80 CGGGAGGCTG GGGGGCCGGG GCCGGGGCCG TGCCCGGAGC GGGTCGGAGG CCGGGGCCGG 900
81 GGCCGGGGGA CGCGGCTCC CCGCGCGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC 960
82 GCAGGGACC ATG GCA GCC GGG AGC ATC ACC ACG CTG CCC GCC TTG CCC GAG 1011
83 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu
84 1 5 10
86 GAT GGC GGC AGC GGC GCC TTC CCG CCC GGC CAC TTC AAG GAC CCC AAG 1059
87 Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys
88 15 20 25 30
90 CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC 1107
91 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp
92 35 40 45
94 GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA 1155
95 Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu
96 50 55 60
98 CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203
99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys
100 65 70 75
102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 1251
103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser
104 80 85 90
106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299
107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn
108 95 100 105 110
110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347
111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala
112 115 120 125
114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395
115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly
116 130 135 140
118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446
119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
120 145 150 155
122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506
123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTATATCC 1566
124 AGTAGTAAAA TATGTAACCA TGCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626
125 TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT 1686

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126 TTTCACGCAT TTGCTTTATT CGAAAAGAGG CTTTAAAAAT GTGCATGTTT AGAAAACAAA 1746
127 ATTTCTTCAT GGAAATCATA TACATTAGAA AATCACAGTC AGATGTTTAA TCAATCCAAA 1806
128 AATGTCCACT ATTTCTTATG TCATTTCGTTA GTCTACATGT TTCTAAACAT ATAAATGTGA 1866
129 ATTTAATCAA TTCCTTTCAT AGTTTTATAA TTCTCTGGCA GTTCCTTATG ATAGAGTTTA 1926
130 TAAAACAGTC CTGTGTAAAC TGCTGGAAGT TCTTCCGGAA TTC 1969

```

132 (2) INFORMATION FOR SEQ ID NO: 2:

134 (i) SEQUENCE CHARACTERISTICS:

135 (A) LENGTH: 155 amino acids

136 (B) TYPE: amino acid

137 (C) STRANDEDNESS: single

138 (D) TOPOLOGY: linear

140 (ii) MOLECULE TYPE: protein

141 (v) FRAGMENT TYPE: internal

143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

145 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
146 1 5 10 15
147 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
148 20 25 30
149 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
150 35 40 45
151 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
152 50 55 60
153 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
154 65 70 75 80
155 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
156 85 90 95
157 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
158 100 105 110
159 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
160 115 120 125
161 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
162 130 135 140
163 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
164 145 150 155

```

166 (2) INFORMATION FOR SEQ ID NO: 3:

168 (i) SEQUENCE CHARACTERISTICS:

169 (A) LENGTH: 638 base pairs

170 (B) TYPE: nucleic acid

171 (C) STRANDEDNESS: double

172 (D) TOPOLOGY: linear

174 (ii) MOLECULE TYPE: cDNA

175 (ix) FEATURE:

177 (A) NAME/KEY: Coding Sequence

178 (B) LOCATION: 91...555

179 (D) OTHER INFORMATION:

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

183 TGCATTTTGT GCCTTTGCTG GAAGAACCGA CTACAGGTTT GTTCAATTC TTACAGTCTT 60
184 GAAAGCGCCA CAAGCAGCAG CTGCTGAGCC ATG GCT GAA GGG GAA ATC ACC ACC 114
185 Met Ala Glu Gly Glu Ile Thr Thr

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186                                     1                                     5
188 TTC ACA GCC CTG ACC GAG AAG TTT AAT CTG CCT CCA GGG AAT TAC AAG      162
189 Phe Thr Ala Leu Thr Glu Lys Phe Asn Leu Pro Pro Gly Asn Tyr Lys
190      10                        15                        20
192 AAG CCC AAA CTC CTC TAC TGT AGC AAC GGG GGC CAC TTC CTG AGG ATC      210
193 Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile
194      25                        30                        35                        40
196 CTT CCG GAT GGC ACA GTG GAT GGG ACA AGG GAC AGG AGC GAC CAG CAC      258
197 Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His
198      45                        50                        55
200 ATT CAG CTG CAG CTC AGT GCG GAA AGC GTG GGG GAG GTG TAT ATA AAG      306
201 Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys
202      60                        65                        70
204 AGT ACC GAG ACT GGC CAG TAC TTG GCC ATG GAC ACC GAC GGG CTT TTA      354
205 Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu
206      75                        80                        85
208 TAC GGC TCA CAG ACA CCA AAT GAG GAA TGT TTG TTC CTG GAA AGG CTG      402
209 Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu
210      90                        95                        100
212 GAG GAG AAC CAT TAC AAC ACC TAT ATA TCC AAG AAG CAT GCA GAG AAG      450
213 Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys
214      105                       110                       115                       120
216 AAT TGG TTT GTT GGC CTC AAG AAG AAT GGG AGC TGC AAA CGC GGT CCT      498
217 Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro
218      125                       130                       135
220 CGG ACT CAC TAT GGC CAG AAA GCA ATC TTG TTT CTC CCC CTG CCA GTC      546
221 Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val
222      140                       145                       150
224 TCT TCT GAT TAAAGAGATC TGTTCTGGGT GTTGACCACT CCAGAGAAGT TTCGAGGGG      604
225 Ser Ser Asp
226      155
228 TCCTCACCTG GTTGACCCAA AAATGTTCCC TTGA      638
230 (2) INFORMATION FOR SEQ ID NO: 4:
232 (i) SEQUENCE CHARACTERISTICS:
233 (A) LENGTH: 155 amino acids
234 (B) TYPE: amino acid
235 (C) STRANDEDNESS: single
236 (D) TOPOLOGY: linear
238 (ii) MOLECULE TYPE: protein
239 (v) FRAGMENT TYPE: internal
241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
243 Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
244      1                        5                        10                        15
245 Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
246      20                        25                        30
247 Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
248      35                        40                        45
249 Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
250      50                        55                        60

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```

251 Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
252 65              70              75              80
253 Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
254              85              90              95
255 Glu Cys Leu Phe Leu Glu Arg Leu Glu Asn His Tyr Asn Thr Tyr
256 100            105            110
257 Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
258 115            120            125
259 Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
260 130            135            140
261 Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
262 145            150            155
264 (2) INFORMATION FOR SEQ ID NO: 5:
266     (i) SEQUENCE CHARACTERISTICS:
267         (A) LENGTH: 103 base pairs
268         (B) TYPE: nucleic acid
269         (C) STRANDEDNESS: single
270         (D) TOPOLOGY: linear
273     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
275 AGAATTCAAA TATTCTGAAA TGAGCTGTTG ACAATTAATC ATCGAACTAG TTAAGTAGTA      60
276 CGCAAGTTCA CGTAAAAAGG GTATCACATA TGGTACCTGC AGA                      103
278 (2) INFORMATION FOR SEQ ID NO: 6:
280     (i) SEQUENCE CHARACTERISTICS:
281         (A) LENGTH: 103 base pairs
282         (B) TYPE: nucleic acid
283         (C) STRANDEDNESS: single
284         (D) TOPOLOGY: linear
287     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
289 TCTGCAGGTA CCATATGTGA TACCCTTTTT ACGTGAAGTT GCGTACTAGT TAACTAGTTC      60
290 GATGATTAAT TGTCAACAGC TCATTTCAGA ATATTGGAAT TCT                      103
292 (2) INFORMATION FOR SEQ ID NO: 7:
294     (i) SEQUENCE CHARACTERISTICS:
295         (A) LENGTH: 16 base pairs
296         (B) TYPE: nucleic acid
297         (C) STRANDEDNESS: single
298         (D) TOPOLOGY: linear
301     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
303 GAAATACACC AGTTGG                      16
305 (2) INFORMATION FOR SEQ ID NO: 8:
307     (i) SEQUENCE CHARACTERISTICS:
308         (A) LENGTH: 17 base pairs
309         (B) TYPE: nucleic acid
310         (C) STRANDEDNESS: single
311         (D) TOPOLOGY: linear
314     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
316 ACTTGATCC AAAACAG                      17
318 (2) INFORMATION FOR SEQ ID NO: 9:
320     (i) SEQUENCE CHARACTERISTICS:
321         (A) LENGTH: 25 base pairs

```

VERIFICATION SUMMARY

DATE: 12/10/2001

PATENT APPLICATION: US/09/902,460

TIME: 11:25:52

Input Set : N:\Crf3\RULE60\09902460.txt

Output Set: N:\CRF3\12102001\I902460.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]